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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=8; day=14; hr=17; min=59; sec=56; ms=479;]

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Reviewer Comments:

<120> DNA Dependent Protein Kinase Catalytic Subunit Phosphorylation Sites and Antibodies Thereto

The above <120> response exceeds the Sequence Rules' required 72-character line limit. Please adjust the line.

(end of Sequence 28)

<400> 28

gccctgggag gcctggtcct ccacaaacat cgga

34

1

Please remove the "1" above, which appears at the end of the submitted file.

Application No: 10511561

Version No: 2.0

Input Set:

Output Set:

Started: 2008-07-15 10:09:22.243
Finished: 2008-07-15 10:09:29.298
Elapsed: 0 hr(s) 0 min(s) 7 sec(s) 55 ms
Total Warnings: 26
Total Errors: 31
No. of SeqIDs Defined: 28
Actual SeqID Count: 28

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
E 257	Invalid sequence data feature in <221> in SEQ ID (1)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
E 257	Invalid sequence data feature in <221> in SEQ ID (2)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
E 257	Invalid sequence data feature in <221> in SEQ ID (4)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
E 257	Invalid sequence data feature in <221> in SEQ ID (5)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 257	Invalid sequence data feature in <221> in SEQ ID (6)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
E 257	Invalid sequence data feature in <221> in SEQ ID (7)

Input Set:

Output Set:

Started: 2008-07-15 10:09:22.243
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Error code	Error Description
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
E 257	Invalid sequence data feature in <221> in SEQ ID (8)
E 257	Invalid sequence data feature in <221> in SEQ ID (8)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (8)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
E 257	Invalid sequence data feature in <221> in SEQ ID (9)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
E 257	Invalid sequence data feature in <221> in SEQ ID (10)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
E 257	Invalid sequence data feature in <221> in SEQ ID (11)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
E 257	Invalid sequence data feature in <221> in SEQ ID (12)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (12)

Input Set:

Output Set:

Started: 2008-07-15 10:09:22.243
Finished: 2008-07-15 10:09:29.298
Elapsed: 0 hr(s) 0 min(s) 7 sec(s) 55 ms
Total Warnings: 26
Total Errors: 31
No. of SeqIDs Defined: 28
Actual SeqID Count: 28

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
E 257	Invalid sequence data feature in <221> in SEQ ID (13)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
E 257	Invalid sequence data feature in <221> in SEQ ID (14)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22) This error has occurred more than 20 times, will not be displayed
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (28)

SEQUENCE LISTING

<110> Chan, Doug W
Chen, Ping-Chi B
Chen, David J

<120> DNA Dependent Protein Kinase Catalytic Subunit Phosphorylation Sites and Antibodies
Thereto

<130> IB-1807 PCT

<140> 10511561

<141> 2008-07-15

<150> US 60/375,094

<151> 2002-04-22

<160> 28

<170> PatentIn version 3.1

<210> 1

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)..(13)

<223> HUMAN GENETIC ORIGIN

<220>

<221> MOD_RES

<222> (6)..(6)

<223> PHOSPHORYLATION at T2609

<400> 1

Pro Met Phe Val Glu Thr Gln Ala Ser Gln Gly Thr Cys
1 5 10

<210> 2

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1)..(14)

<223> HUMAN GENETIC ORIGIN

<220>

<221> MOD_RES
<222> (7)..(7)
<223> PHOSPHORYLATION at S2056

<400> 2

Gln Ser Tyr Ser Tyr Ser Ser Gln Asp Pro Arg Pro Ala Cys
1 5 10

<210> 3

<211> 4128
<212> PRT
<213> Homo sapiens

<400> 3

Met Ala Gly Ser Gly Ala Gly Val Arg Cys Ser Leu Leu Arg Leu Gln
1 5 10 15

Glu Thr Leu Ser Ala Ala Asp Arg Cys Gly Ala Ala Leu Ala Gly His
20 25 30

Gln Leu Ile Arg Gly Leu Gly Gln Glu Cys Val Leu Ser Ser Ser Pro
35 40 45

Ala Val Leu Ala Leu Gln Thr Ser Leu Val Phe Ser Arg Asp Phe Gly
50 55 60

Leu Leu Val Phe Val Arg Lys Ser Leu Asn Ser Ile Glu Phe Arg Glu
65 70 75 80

Cys Arg Glu Glu Ile Leu Lys Phe Leu Cys Ile Phe Leu Glu Lys Met
85 90 95

Gly Gln Lys Ile Ala Pro Tyr Ser Val Glu Ile Lys Asn Thr Cys Thr
100 105 110

Ser Val Tyr Thr Lys Asp Arg Ala Ala Lys Cys Lys Ile Pro Ala Leu
115 120 125

Asp Leu Leu Ile Lys Leu Leu Gln Thr Phe Arg Ser Ser Arg Leu Met
130 135 140

Asp Glu Phe Lys Ile Gly Glu Leu Phe Ser Lys Phe Tyr Gly Glu Leu
145 150 155 160

Ala	Leu	Lys	Lys	Lys	Ile	Pro	Asp	Thr	Val	Leu	Glu	Lys	Val	Tyr	Glu	165	170	175	
Leu	Leu	Gly	Leu	Leu	Gly	Glu	Val	His	Pro	Ser	Glu	Met	Ile	Asn	Asn	180	185	190	
Ala	Glu	Asn	Leu	Phe	Arg	Ala	Phe	Leu	Gly	Glu	Leu	Lys	Thr	Gln	Met	195	200	205	
Thr	Ser	Ala	Val	Arg	Glu	Pro	Lys	Leu	Pro	Val	Leu	Ala	Gly	Cys	Leu	210	215	220	
Lys	Gly	Leu	Ser	Ser	Leu	Leu	Cys	Asn	Phe	Thr	Lys	Ser	Met	Glu	Glu	225	230	235	240
Asp	Pro	Gln	Thr	Ser	Arg	Glu	Ile	Phe	Asn	Phe	Val	Leu	Lys	Ala	Ile	245	250	255	
Arg	Pro	Gln	Ile	Asp	Leu	Lys	Arg	Tyr	Ala	Val	Pro	Ser	Ala	Gly	Leu	260	265	270	
Arg	Leu	Phe	Ala	Leu	His	Ala	Ser	Gln	Phe	Ser	Thr	Cys	Leu	Leu	Asp	275	280	285	
Asn	Tyr	Val	Ser	Leu	Phe	Glu	Val	Leu	Leu	Lys	Trp	Cys	Ala	His	Thr	290	295	300	
Asn	Val	Glu	Leu	Lys	Lys	Ala	Ala	Leu	Ser	Ala	Leu	Glu	Ser	Phe	Leu	305	310	315	320
Lys	Gln	Val	Ser	Asn	Met	Val	Ala	Lys	Asn	Ala	Glu	Met	His	Lys	Asn	325	330	335	
Lys	Leu	Gln	Tyr	Phe	Met	Glu	Gln	Phe	Tyr	Gly	Ile	Ile	Arg	Asn	Val	340	345	350	
Asp	Ser	Asn	Asn	Lys	Glu	Leu	Ser	Ile	Ala	Ile	Arg	Gly	Tyr	Gly	Leu	355	360	365	
Phe	Ala	Gly	Pro	Cys	Lys	Val	Ile	Asn	Ala	Lys	Asp	Val	Asp	Phe	Met	370	375	380	

Tyr Val Glu Leu Ile Gln Arg Cys Lys Gln Met Phe Leu Thr Gln Thr
385 390 395 400

Asp Thr Gly Asp Tyr Arg Val Tyr Gln Met Pro Ser Phe Leu Gln Ser
405 410 415

Val Ala Ser Val Leu Leu Tyr Leu Asp Thr Val Pro Glu Val Tyr Thr
420 425 430

Pro Val Leu Glu His Leu Val Val Met Gln Ile Asp Ser Phe Pro Gln
435 440 445

Tyr Ser Pro Lys Met Gln Leu Val Cys Cys Arg Ala Ile Val Lys Val
450 455 460

Phe Leu Ala Leu Ala Ala Lys Gly Pro Val Leu Arg Asn Cys Ile Ser
465 470 475 480

Thr Val Val His Gln Gly Leu Ile Arg Ile Cys Ser Lys Pro Val Val
485 490 495

Leu Pro Lys Gly Pro Glu Ser Glu Ser Glu Asp His Arg Ala Ser Gly
500 505 510

Glu Val Arg Thr Gly Lys Trp Lys Val Pro Thr Tyr Lys Asp Tyr Val
515 520 525

Asp Leu Phe Arg His Leu Leu Ser Ser Asp Gln Met Met Asp Ser Ile
530 535 540

Leu Ala Asp Glu Ala Phe Phe Ser Val Asn Ser Ser Ser Glu Ser Leu
545 550 555 560

Asn His Leu Leu Tyr Asp Glu Phe Val Lys Ser Val Leu Lys Ile Val
565 570 575

Glu Lys Leu Asp Leu Thr Leu Glu Ile Gln Thr Val Gly Glu Gln Glu
580 585 590

Asn Gly Asp Glu Ala Pro Gly Val Trp Met Ile Pro Thr Ser Asp Pro
595 600 605

Ala Ala Asn Leu His Pro Ala Lys Pro Lys Asp Phe Ser Ala Phe Ile

610	615	620
Asn Leu Val Glu Phe Cys Arg Glu Ile Leu Pro Glu Lys Gln Ala Glu		
625	630	635 640
Phe Phe Glu Pro Trp Val Tyr Ser Phe Ser Tyr Glu Leu Ile Leu Gln		
645	650	655
Ser Thr Arg Leu Pro Leu Ile Ser Gly Phe Tyr Lys Leu Leu Ser Ile		
660	665	670
Thr Val Arg Asn Ala Lys Lys Ile Lys Tyr Phe Glu Gly Val Ser Pro		
675	680	685
Lys Ser Leu Lys His Ser Pro Glu Asp Pro Glu Lys Tyr Ser Cys Phe		
690	695	700
Ala Leu Phe Val Lys Phe Gly Lys Glu Val Ala Val Lys Met Lys Gln		
705	710	715 720
Tyr Lys Asp Glu Leu Leu Ala Ser Cys Leu Thr Phe Leu Leu Ser Leu		
725	730	735
Pro His Asn Ile Ile Glu Leu Asp Val Arg Ala Tyr Val Pro Ala Leu		
740	745	750
Gln Met Ala Phe Lys Leu Gly Leu Ser Tyr Thr Pro Leu Ala Glu Val		
755	760	765
Gly Leu Asn Ala Leu Glu Glu Trp Ser Ile Tyr Ile Asp Arg His Val		
770	775	780
Met Gln Pro Tyr Tyr Lys Asp Ile Leu Pro Cys Leu Asp Gly Tyr Leu		
785	790	795 800
Lys Thr Ser Ala Leu Ser Asp Glu Thr Lys Asn Asn Trp Glu Val Ser		
805	810	815
Ala Leu Ser Arg Ala Ala Gln Lys Gly Phe Asn Lys Val Val Leu Lys		
820	825	830
His Leu Lys Lys Thr Lys Asn Leu Ser Ser Asn Glu Ala Ile Ser Leu		
835	840	845

Glu Glu Ile Arg Ile Arg Val Val Gln Met Leu Gly Ser Leu Gly Gly
850 855 860

Gln Ile Asn Lys Asn Leu Leu Thr Val Thr Ser Ser Asp Glu Met Met
865 870 875 880

Lys Ser Tyr Val Ala Trp Asp Arg Glu Lys Arg Leu Ser Phe Ala Val
885 890 895

Pro Phe Arg Glu Met Lys Pro Val Ile Phe Leu Asp Val Phe Leu Pro
900 905 910

Arg Val Thr Glu Leu Ala Leu Thr Ala Ser Asp Arg Gln Thr Lys Val
915 920 925

Ala Ala Cys Glu Leu Leu His Ser Met Val Met Phe Met Leu Gly Lys
930 935 940

Ala Thr Gln Met Pro Glu Gly Gly Gln Gly Ala Pro Pro Met Tyr Gln
945 950 955 960

Leu Tyr Lys Arg Thr Phe Pro Val Leu Leu Arg Leu Ala Cys Asp Val
965 970 975

Asp Gln Val Thr Arg Gln Leu Tyr Glu Pro Leu Val Met Gln Leu Ile
980 985 990

His Trp Phe Thr Asn Asn Lys Lys Phe Glu Ser Gln Asp Thr Val Ser
995 1000 1005

Leu Leu Glu Ala Ile Leu Asp Gly Ile Val Asp Pro Val Asp Ser
1010 1015 1020

Thr Leu Arg Asp Phe Cys Gly Arg Cys Ile Arg Glu Phe Leu Lys
1025 1030 1035

Trp Ser Ile Lys Gln Ile Thr Pro Gln Gln Gln Glu Lys Ser Pro
1040 1045 1050

Val Asn Thr Lys Ser Leu Phe Lys Arg Leu Tyr Ser Leu Ala Leu
1055 1060 1065

His Pro	Asn Ala Phe Lys Arg	Leu Gly Ala Ser Leu	Ala Phe Asn
1070	1075	1080	
Asn Ile	Tyr Arg Glu Phe Arg	Glu Glu Glu Ser Leu	Val Glu Gln
1085	1090	1095	
Phe Val	Phe Glu Ala Leu Val	Ile Tyr Met Glu Ser	Leu Ala Leu
1100	1105	1110	
Ala His	Ala Asp Glu Lys Ser	Leu Gly Thr Ile Gln	Gln Cys Cys
1115	1120	1125	
Asp Ala	Ile Asp His Leu Cys	Arg Ile Ile Glu Lys	Lys His Val
1130	1135	1140	
Ser Leu	Asn Lys Ala Lys Lys	Arg Arg Leu Pro Arg	Gly Phe Pro
1145	1150	1155	
Pro Ser	Ala Ser Leu Cys Leu	Leu Asp Leu Val Lys	Trp Leu Leu
1160	1165	1170	
Ala His	Cys Gly Arg Pro Gln	Thr Glu Cys Arg His	Lys Ser Ile
1175	1180	1185	
Glu Leu	Phe Tyr Lys Phe Val	Pro Leu Leu Pro Gly	Asn Arg Ser
1190	1195	1200	
Pro Asn	Leu Trp Leu Lys Asp	Val Leu Lys Glu Glu	Gly Val Ser
1205	1210	1215	
Phe Leu	Ile Asn Thr Phe Glu	Gly Gly Gly Cys Gly	Gln Pro Ser
1220	1225	1230	
Gly Ile	Leu Ala Gln Pro Thr	Leu Leu Tyr Leu Arg	Gly Pro Phe
1235	1240	1245	
Ser Leu	Gln Ala Thr Leu Cys	Trp Leu Asp Leu Leu	Leu Ala Ala
1250	1255	1260	
Leu Glu	Cys Tyr Asn Thr Phe	Ile Gly Glu Arg Thr	Val Gly Ala
1265	1270	1275	

Leu Gln Val Leu Gly Thr Glu Ala Gln Ser Ser Leu Leu Lys Ala
1280 1285 1290

Val Ala Phe Phe Leu Glu Ser Ile Ala Met His Asp Ile Ile Ala
1295 1300 1305

Ala Glu Lys Cys Phe Gly Thr Gly Ala Ala Gly Asn Arg Thr Ser
1310 1315 1320

Pro Gln Glu Gly Glu Arg Tyr Asn Tyr Ser Lys Cys Thr Val Val
1325 1330 1335

Val Arg Ile Met Glu Phe Thr Thr Thr Leu Leu Asn Thr Ser Pro
1340 1345 1350

Glu Gly Trp Lys Leu Leu Lys Lys Asp Leu Cys Asn Thr His Leu
1355 1360 1365

Met Arg Val Leu Val Gln Thr Leu Cys Glu Pro Ala Ser Ile Gly
1370 1375 1380

Phe Asn Ile Gly Asp Val Gln Val Met Ala His Leu Pro Asp Val
1385 1390 1395

Cys Val Asn Leu Met Lys Ala Leu Lys Met Ser Pro Tyr Lys Asp
1400 1405 1410

Ile Leu Glu Thr His Leu Arg Glu Lys Ile Thr Ala Gln Ser Ile
1415 1420 1425

Glu Glu Leu Cys Ala Val Asn Leu Tyr Gly Pro Asp Ala Gln Val
1430 1435 1440

Asp Arg Ser Arg Leu Ala Ala Val Val Ser Ala Cys Lys Gln Leu
1445 1450 1455

His Arg Ala Gly Leu Leu His Asn Ile Leu Pro Ser Gln Ser Thr
1460 1465 1470

Asp Leu His His Ser Val Gly Thr Glu Leu Leu Ser Leu Val Tyr
1475 1480 1485

Lys Gly Ile Ala Pro Gly Asp Glu Arg Gln Cys Leu Pro Ser Leu

1490		1495		1500
Asp Leu Ser Cys Lys Gln Leu Ala Ser Gly Leu Leu Glu Leu Ala				
1505		1510		1515
Phe Ala Phe Gly Gly Leu Cys Glu Arg Leu Val Ser Leu Leu Leu				
1520		1525		1530
Asn Pro Ala Val Leu Ser Thr Ala Ser Leu Gly Ser Ser Gln Gly				
1535		1540		1545
Ser Val Ile His Phe Ser His Gly Glu Tyr Phe Tyr Ser Leu Phe				
1550		1555		1560
Ser Glu Thr Ile Asn Thr Glu Leu Leu Lys Asn Leu Asp Leu Ala				
1565		1570		1575
Val Leu Glu Leu Met Gln Ser Ser Val Asp Asn Thr Lys Met Val				
1580		1585		1590
Ser Ala Val Leu Asn Gly Met Leu Asp Gln Ser Phe Arg Glu Arg				
1595		1600		1605
Ala Asn Gln Lys His Gln Gly Leu Lys Leu Ala Thr Thr Ile Leu				
1610		1615		1620
Gln His Trp Lys Lys Cys Asp Ser Trp Trp Ala Lys Asp Ser Pro				
1625		1630		1635
Leu Glu Thr Lys Met Ala Val Leu Ala Leu Leu Ala Lys Ile Leu				
1640		1645		1650
Gln Ile Asp Ser Ser Val Ser Phe Asn Thr Ser His Gly Ser Phe				
1655		1660		1665
Pro Glu Val Phe Thr Thr Tyr Ile Ser Leu Leu Ala Asp Thr Lys				
1670		1675		1680
Leu Asp Leu His Leu Lys Gly Gln Ala Val Thr Leu Leu Pro Phe				
1685		1690		1695
Phe Thr Ser Leu Thr Gly Gly Ser Leu Glu Glu Leu Arg Arg Val				
1700		1705		1710

Leu Glu Gln Leu Ile Val Ala His Phe Pro Met Gln Ser Arg Glu
1715 1720 1725

Phe Pro Pro Gly Thr Pro Arg Phe Asn Asn Tyr Val Asp Cys Met
1730 1735 1740

Lys Lys Phe Leu Asp Ala Leu Glu Leu Ser Gln Ser Pro Met Leu
1745 1750 1755

Leu Glu Leu Met Thr Glu Val Leu Cys Arg Glu Gln Gln His Val
1760 1765 1770

Met Glu Glu Leu Phe Gln Ser Ser Phe Arg Arg Ile Ala Arg Arg
1775 1780 1785

Gly Ser Cys Val Thr Gln Val Gly Leu Leu Glu Ser Val Tyr Glu
1790 1795 1800

Met Phe Arg Lys Asp Asp Pro Arg Leu Ser Phe Thr Arg Gln Ser
1805 1810 1815

Phe Val Asp Arg Ser Leu Leu Thr Leu Leu Trp His Cys Ser Leu
1820 1825 1830

Asp Ala Leu Arg Glu Phe Phe Ser Thr Ile Val Val Asp Ala Ile
1835 1840 1845

Asp Val Leu Lys Ser Arg Phe Thr Lys Leu Asn Glu Ser Thr Phe
1850 1855 1860

Asp Thr Gln Ile Thr Lys Lys Met Gly Tyr Tyr Lys Ile Leu Asp
1865 1870 1875

Val Met Tyr Ser Arg Leu Pro Lys Asp Asp Val His Ala Lys Glu
1880 1885 1890

Ser Lys Ile Asn Gln Val Phe His Gly Ser Cys Ile Thr Glu Gly
1895 1900 1905

Asn Glu Leu Thr Ly